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SEQUENCE LISTING

<110> Fleckenstein, Annette E.
Hanson, Glen R.

<120> MODULATING VESICULAR MONOAMINE TRANSPORTER
TRAFFICKING AND FUNCTION: A NOVEL APPROACH FOR
THE TREATMENT OF PARKINSON'S DISEASE

<130> 21101.0031U3

<150> PCT/US03/29668

<151> 2003-09-19

<150> 60/412,439

<151> 2002-09-19

<160> 18

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 515

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 1

Met	Ala	Leu	Ser	Asp	Leu	Val	Leu	Leu	Arg	Trp	Leu	Arg	Asp	Ser	Arg	1	5	10	15
His	Ser	Arg	Lys	Leu	Ile	Leu	Phe	Ile	Val	Phe	Leu	Ala	Leu	Leu	Leu	20	25	30	
Asp	Asn	Met	Leu	Leu	Thr	Val	Val	Pro	Ile	Ile	Pro	Ser	Tyr	Leu		35	40	45	
Tyr	Ser	Ile	Lys	His	Glu	Lys	Asn	Ser	Thr	Glu	Ile	Gln	Thr	Thr	Arg	50	55	60	
Pro	Glu	Leu	Val	Val	Ser	Thr	Ser	Glu	Ser	Ile	Phe	Ser	Tyr	Tyr	Asn	65	70	75	80
Asn	Ser	Thr	Val	Leu	Ile	Thr	Gly	Asn	Ala	Thr	Gly	Thr	Leu	Pro	Gly	85	90	95	
Gly	Gln	Ser	His	Lys	Ala	Thr	Ser	Thr	Gln	His	Thr	Val	Ala	Asn	Thr	100	105	110	
Thr	Val	Pro	Ser	Asp	Cys	Pro	Ser	Glu	Asp	Arg	Asp	Leu	Leu	Asn	Glu	115	120	125	
Asn	Val	Gln	Val	Gly	Leu	Leu	Phe	Ala	Ser	Lys	Ala	Thr	Val	Gln	Leu	130	135	140	
Leu	Thr	Asn	Pro	Phe	Ile	Gly	Leu	Leu	Thr	Asn	Arg	Ile	Gly	Tyr	Pro	145	150	155	160
Ile	Pro	Met	Phe	Ala	Gly	Phe	Cys	Ile	Met	Phe	Ile	Ser	Thr	Val	Met	165	170	175	
Phe	Ala	Phe	Ser	Ser	Tyr	Ala	Phe	Leu	Leu	Ile	Ala	Arg	Ser	Leu		180	185	190	
Gln	Gly	Ile	Gly	Ser	Ser	Cys	Ser	Val	Ala	Gly	Met	Gly	Met	Leu		195	200	205	
Ala	Ser	Val	Tyr	Thr	Asp	Asp	Glu	Glu	Arg	Gly	Asn	Ala	Met	Gly	Ile	210	215	220	
Ala	Leu	Gly	Gly	Leu	Ala	Met	Gly	Val	Leu	Val	Gly	Pro	Pro	Phe	Gly	225	230	235	240

Ser Val Leu Tyr Glu Phe Val Gly Lys Thr Ala Pro Phe Leu Val Leu
 245 250 255
 Ala Ala Leu Val Leu Leu Asp Gly Ala Ile Gln Leu Phe Val Leu Gln
 260 265 270
 Pro Ser Arg Val Gln Pro Glu Ser Gln Lys Gly Thr Pro Leu Thr Thr
 275 280 285
 Leu Leu Lys Asp Pro Tyr Ile Leu Ile Ala Ala Gly Ser Ile Cys Phe
 290 295 300
 Ala Asn Met Gly Ile Ala Met Leu Glu Pro Ala Leu Pro Ile Trp Met
 305 310 315 320
 Met Glu Thr Met Cys Ser Arg Lys Trp Gln Leu Gly Val Ala Phe Leu
 325 330 335
 Pro Ala Ser Ile Ser Tyr Leu Ile Gly Thr Asn Ile Phe Gly Ile Leu
 340 345 350
 Ala His Lys Met Gly Arg Trp Leu Cys Ala Leu Leu Gly Met Val Ile
 355 360 365
 Val Gly Ile Ser Ile Leu Cys Ile Pro Phe Ala Lys Asn Ile Tyr Gly
 370 375 380
 Leu Ile Ala Pro Asn Phe Gly Val Gly Phe Ala Ile Gly Met Val Asp
 385 390 395 400
 Ser Ser Met Met Pro Ile Met Gly Tyr Leu Val Asp Leu Arg His Val
 405 410 415
 Ser Val Tyr Gly Ser Val Tyr Ala Ile Ala Asp Val Ala Phe Cys Met
 420 425 430
 Gly Tyr Ala Ile Gly Pro Ser Ala Gly Gly Ala Ile Ala Lys Ala Ile
 435 440 445
 Gly Phe Pro Trp Leu Met Thr Ile Ile Gly Ile Ile Asp Ile Ala Phe
 450 455 460
 Ala Pro Leu Cys Phe Phe Leu Arg Ser Pro Pro Ala Lys Glu Glu Lys
 465 470 475 480
 Met Ala Ile Leu Met Asp His Asn Cys Pro Ile Lys Thr Lys Met Tyr
 485 490 495
 Thr Gln Asn Asn Val Gln Ser Tyr Pro Ile Gly Asp Asp Glu Glu Ser
 500 505 510
 Glu Ser Asp
 515

<210> 2

<211> 1548

<212> DNA

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 2

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ctgatcctgt	tcatcgtgtt	ccttgcgctg	ctgctggaca	acatgctgct	caccgctcgtg	120
gttcccatca	tcccagcta	tctgtacagc	attaagcatg	agaaaaactc	tacggaaatc	180
cagaccacca	gaccagagct	cgtgggtctcc	acctccgaaa	gcatcttctc	ttactataac	240
aactctactg	tggtgatcac	cgggaatgcc	actgggactc	ttccaggagg	gcagtcacac	300
aaggctacca	gcacacagca	cactgtggct	aacaccactg	tcccttcgga	ctgtccagct	360
gaagacagag	accttctgaa	tgagaatgtg	caagtggggc	tgctgtttgc	ctccaaagcc	420
actgtccagc	tcctcactaa	cccattcata	ggacttctga	ccaacagaat	tggttatcca	480
attcccatgt	ttgcgggctt	ctgcatcatg	tttatctcaa	cagttatggt	tgcccttctcc	540
agcagctatg	ccttcctgct	gatcgccagg	tcccttcagg	gaattggctc	ctcctgctca	600
tccgtggctg	ggatgggtat	gctggccagc	gtgtacacag	atgatgagga	gagggggaac	660
gccatgggca	ttgctttggg	tggcctggcc	atggggagtct	tagtgggacc	ccccttcggg	720
agtgtgctct	atgagtttgt	ggggaagaca	gctcccttcc	tggtgctagc	tgcccttggtg	780
ctcttggtatg	gggctattca	gctctttgtg	ctccagccgt	cccagagtaca	gccagagagt	840

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cagaagggga cacctctaac gaccttgctg aaggatccat acatcctcat cgctgcaggc      900
tccatctgct ttgcaaacat ggggatagcc atgctggagc ccgccctgcc catctggatg      960
atggagacca tgtgttcccg aaagtggcag ctgggcgttg ctttcctccc ggcgagcatc     1020
tcttatctca ttggaaccaa tatttttggg atacttgcac acaaaatggg aaggtggcta     1080
tgtgctcttc tgggaatggt aattgttgga atcagcattt tatgcatccc ctttgcaaaa     1140
aatatctatg gactcatcgc tcccaacttt ggagttggtt ttgcaattgg gatgggtggac     1200
tcctctatga tgcctatcat gggctacctg gttgacctgc ggcattgtgtc tgtctatggg     1260
agtgtttatg ccattgcaga cgtggccttt tgtatgggct atgctatcgg tccctctgct     1320
gggtggtgcca tcgcaaaggc aattggcttt ccttggctta tgacaattat tgggataatt     1380
gatatcgctt ttgctccact ctgctttttc cttcgaagtc cacctgctaa ggaggaaaaa     1440
atggctatcc tcatggacca caactgtccc attaaaacaa agatgtacac tcagaataat     1500
gtccagtcac atcccatcgg tgatgatgaa gaatctgaaa gtgactga      1548

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<210> 3

<211> 514

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 3

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Met Ala Leu Ser Glu Leu Ala Leu Val Arg Trp Leu Gln Glu Ser Arg
 1              5              10              15
His Ser Arg Lys Leu Ile Leu Phe Ile Val Phe Leu Ala Leu Leu Leu
      20              25              30
Asp Asn Met Leu Leu Thr Val Val Val Pro Ile Ile Pro Ser Tyr Leu
      35              40              45
Tyr Ser Ile Lys His Glu Lys Asn Ala Thr Glu Ile Gln Thr Ala Arg
      50              55              60
Pro Val His Thr Ala Ser Ile Ser Asp Ser Phe Gln Ser Ile Phe Ser
      65              70              75              80
Tyr Tyr Asp Asn Ser Thr Met Val Thr Gly Asn Ala Thr Arg Asp Leu
      85              90              95
Thr Leu His Gln Thr Ala Thr Gln His Met Val Thr Asn Ala Ser Ala
      100             105             110
Val Pro Ser Asp Cys Pro Ser Glu Asp Lys Asp Leu Leu Asn Glu Asn
      115             120             125
Val Gln Val Gly Leu Leu Phe Ala Ser Lys Ala Thr Val Gln Leu Ile
      130             135             140
Thr Asn Pro Phe Ile Gly Leu Leu Thr Asn Arg Ile Gly Tyr Pro Ile
      145             150             155             160
Pro Ile Phe Ala Gly Phe Cys Ile Met Phe Val Ser Thr Ile Met Phe
      165             170             175
Ala Phe Ser Ser Ser Tyr Ala Phe Leu Ile Ala Arg Ser Leu Gln
      180             185             190
Gly Ile Gly Ser Ser Cys Ser Ser Val Ala Gly Met Gly Met Leu Ala
      195             200             205
Ser Val Tyr Thr Asp Asp Glu Glu Arg Gly Asn Val Met Gly Ile Ala
      210             215             220
Leu Gly Gly Leu Ala Met Gly Val Leu Val Gly Pro Pro Phe Gly Ser
      225             230             235             240
Val Leu Tyr Glu Phe Val Gly Lys Thr Ala Pro Phe Leu Val Leu Ala
      245             250             255
Ala Leu Val Leu Leu Asp Gly Ala Ile Gln Leu Phe Val Leu Gln Pro
      260             265             270
Ser Arg Val Gln Pro Glu Ser Gln Lys Gly Thr Pro Leu Thr Thr Leu
      275             280             285
Leu Lys Asp Pro Tyr Ile Leu Ile Ala Ala Gly Ser Ile Cys Phe Ala
      290             295             300

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Asn Met Gly Ile Ala Met Leu Glu Pro Ala Leu Pro Ile Trp Met Met
 305 310 315 320
 Glu Thr Met Cys Ser Arg Lys Trp Gln Leu Gly Val Ala Phe Leu Pro
 325 330 335
 Ala Ser Ile Ser Tyr Leu Ile Gly Thr Asn Ile Phe Gly Ile Leu Ala
 340 345 350
 His Lys Met Gly Arg Trp Leu Cys Ala Leu Leu Gly Met Ile Ile Val
 355 360 365
 Gly Val Ser Ile Leu Cys Ile Pro Phe Ala Lys Asn Ile Tyr Gly Leu
 370 375 380
 Ile Ala Pro Asn Phe Gly Val Gly Phe Ala Ile Gly Met Val Asp Ser
 385 390 395 400
 Ser Met Met Pro Ile Met Gly Tyr Leu Val Asp Leu Arg His Val Ser
 405 410 415
 Val Tyr Gly Ser Val Tyr Ala Ile Ala Asp Val Ala Phe Cys Met Gly
 420 425 430
 Tyr Ala Ile Gly Pro Ser Ala Gly Gly Ala Ile Ala Lys Ala Ile Gly
 435 440 445
 Phe Pro Trp Leu Met Thr Ile Ile Gly Ile Ile Asp Ile Leu Phe Ala
 450 455 460
 Pro Leu Cys Phe Phe Leu Arg Ser Pro Pro Ala Lys Glu Glu Lys Met
 465 470 475 480
 Ala Ile Leu Met Asp His Asn Cys Pro Ile Lys Thr Lys Met Tyr Thr
 485 490 495
 Gln Asn Asn Ile Gln Ser Tyr Pro Ile Gly Glu Asp Glu Glu Ser Glu
 500 505 510
 Ser Asp

<210> 4

<211> 1545

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 4

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ctcatcctgt	tcacgtgtgt	cctgggcgtg	ctgctggaca	acatgctgct	cactgtcgtg	120
gtccccatca	tcccaagtta	tctgtacagc	attaagcatg	agaagaatgc	tacagaaatc	180
cagacggcca	ggccagtgc	cactgcctcc	atctcagaca	gcttccagag	catcttctcc	240
tattatgata	actcgactat	ggtcaccggg	aatgctacca	gagacctgac	acttcatcag	300
accgccacac	agcacatggt	gaccaacgcg	tccgctgttc	cttccgactg	tcccagtga	360
gacaaagacc	tcctgaatga	aaacgtgcaa	gttgggtctgt	tgtttgcttc	gaaagccacc	420
gtccagctca	tcaccaaccc	tttcatagga	ctactgacca	acagaattgg	ctatccaatt	480
cccatatttg	cgggattctg	catcatgttt	gtctcaacaa	ttatgtttgc	cttctccagc	540
agctatgcct	tcctgctgat	tgccaggctg	ctgcagggca	tcggctcgtc	ctgctcctct	600
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atgggaatcg	ccttggggagg	cctggccatg	ggggctcttag	tgggcccccc	cttcgggagt	720
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aaggggacac	ccctaaccac	gctgctgaag	gacccgtaca	tcctcattgc	tgcaggctcc	900
atctgctttg	caaacatggg	catcgccatg	ctggagccag	ccctgccccat	ctggatgatg	960
gagaccatgt	gttcccga	gtggcagctg	ggcgttgctt	tcttgccagc	tagtatctct	1020
tatctcattg	gaaccaatat	ttttgggata	cttgcacaca	aaatggggag	gtggctttgt	1080
gctcttcttg	gaatgataat	tggtggagtc	agcattttat	gtattccatt	tgcaaaaaac	1140
atcttatggac	tcatagctcc	gaactttgga	gttgggtttg	caattggaat	gggtggattcg	1200
tcaatgatgc	ctatcatggg	ctacctcgta	gacctgcggc	acgtgtccgt	ctatgggagt	1260
gtgtacgcca	ttgcggatgt	ggcattttgt	atgggggtatg	ctataggtcc	ttctgctggt	1320

ggtgctattg	caaaggcaat	tggattttcca	tggctcatga	caattattgg	gataattgat	1380
attctttttg	cccctctctg	cttttttctt	cgaagtccac	ctgccaaaga	agaaaaaatg	1440
gctattctca	tggatcacaa	ctgccctatt	aaaacaaaaa	tgtacactca	gaataatatc	1500
cagtcatatc	cgataggtga	agatgaagaa	tctgaaagtg	actga		1545

<210> 5

<211> 525

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 5

Met	Leu	Arg	Thr	Ile	Leu	Asp	Ala	Pro	Gln	Arg	Leu	Leu	Lys	Glu	Gly
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Arg	Ala	Ser	Arg	Gln	Leu	Val	Leu	Val	Val	Val	Phe	Val	Ala	Leu	Leu
			20					25					30		
Leu	Asp	Asn	Met	Leu	Phe	Thr	Val	Val	Val	Pro	Ile	Val	Pro	Thr	Phe
		35					40					45			
Leu	Tyr	Asp	Met	Glu	Phe	Lys	Glu	Val	Asn	Ser	Ser	Leu	His	Leu	Gly
	50					55					60				
His	Ala	Gly	Ser	Ser	Pro	His	Ala	Leu	Ala	Ser	Pro	Ala	Phe	Ser	Thr
65					70					75					80
Ile	Phe	Ser	Phe	Phe	Asn	Asn	Asn	Thr	Val	Ala	Val	Glu	Glu	Ser	Val
			85					90					95		
Pro	Ser	Gly	Ile	Ala	Trp	Met	Asn	Asp	Thr	Ala	Ser	Thr	Ile	Pro	Pro
			100					105					110		
Pro	Ala	Thr	Glu	Ala	Ile	Ser	Ala	His	Lys	Asn	Asn	Cys	Leu	Gln	Gly
		115					120					125			
Thr	Gly	Phe	Leu	Glu	Glu	Glu	Ile	Thr	Arg	Val	Gly	Val	Leu	Phe	Ala
	130					135					140				
Ser	Lys	Ala	Val	Met	Gln	Leu	Leu	Val	Asn	Pro	Phe	Val	Gly	Pro	Leu
145					150					155					160
Thr	Asn	Arg	Ile	Gly	Tyr	His	Ile	Pro	Met	Phe	Ala	Gly	Phe	Val	Ile
			165						170					175	
Met	Phe	Leu	Ser	Thr	Val	Met	Phe	Ala	Phe	Ser	Gly	Thr	Tyr	Thr	Leu
		180					185						190		
Leu	Phe	Val	Ala	Arg	Thr	Leu	Gln	Gly	Ile	Gly	Ser	Ser	Phe	Ser	Ser
		195					200					205			
Val	Ala	Gly	Leu	Gly	Met	Leu	Ala	Ser	Val	Tyr	Thr	Asp	Asp	His	Glu
	210					215					220				
Arg	Gly	Arg	Ala	Met	Gly	Thr	Ala	Leu	Gly	Gly	Leu	Ala	Leu	Gly	Leu
225				230						235					240
Leu	Val	Gly	Ala	Pro	Phe	Gly	Ser	Val	Met	Tyr	Glu	Phe	Val	Gly	Lys
			245						250					255	
Ser	Ala	Pro	Phe	Leu	Ile	Leu	Ala	Phe	Leu	Ala	Leu	Leu	Asp	Gly	Ala
		260					265						270		
Leu	Gln	Leu	Cys	Ile	Leu	Gln	Pro	Ser	Lys	Val	Ser	Pro	Glu	Ser	Ala
	275					280						285			
Lys	Gly	Thr	Pro	Leu	Phe	Met	Leu	Leu	Lys	Asp	Pro	Tyr	Ile	Leu	Val
	290					295					300				
Ala	Ala	Gly	Ser	Ile	Cys	Phe	Ala	Asn	Met	Gly	Val	Ala	Ile	Leu	Glu
305				310						315					320
Pro	Thr	Leu	Pro	Ile	Trp	Met	Met	Gln	Thr	Met	Cys	Ser	Pro	Lys	Trp
			325						330					335	
Gln	Leu	Gly	Leu	Ala	Phe	Leu	Pro	Ala	Ser	Val	Ser	Tyr	Leu	Ile	Gly
		340					345						350		
Thr	Asn	Leu	Phe	Gly	Val	Leu	Ala	Asn	Lys	Met	Gly	Arg	Trp	Leu	Cys
	355						360					365			

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Ser Leu Ile Gly Met Leu Val Val Gly Thr Ser Leu Leu Cys Val Pro
 370                               375                               380
Leu Ala His Asn Ile Phe Gly Leu Ile Gly Pro Asn Ala Gly Leu Gly
385                               390                               395                               400
Leu Ala Ile Gly Met Val Asp Ser Ser Met Met Pro Ile Met Gly His
                               405                               410                               415
Leu Val Asp Leu Arg His Thr Ser Val Tyr Gly Ser Val Tyr Ala Ile
                               420                               425                               430
Ala Asp Val Ala Phe Cys Met Gly Phe Ala Ile Gly Pro Ser Thr Gly
                               435                               440                               445
Gly Ala Ile Val Lys Ala Ile Gly Phe Pro Trp Leu Met Val Ile Thr
                               450                               455                               460
Gly Val Ile Asn Ile Val Tyr Ala Pro Leu Cys Tyr Tyr Leu Arg Ser
465                               470                               475                               480
Pro Pro Ala Lys Glu Glu Lys Leu Ala Ile Leu Ser Gln Asp Cys Pro
                               485                               490                               495
Met Glu Thr Arg Met Tyr Ala Thr Gln Lys Pro Thr Lys Glu Phe Pro
                               500                               505                               510
Leu Gly Glu Asp Ser Asp Glu Glu Pro Asp His Glu Glu
                               515                               520                               525

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<210> 6

<211> 1578

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 6

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ctgcacctcg gccatgccgg aagttcccca catgccctcg cctctcctgc cttttccacc 240
atcttctcct tcttcaacaa caacaccgtg gctgttgaag aaagcgtacc tagtgaata 300
gcattggtga atgacactgc cagcaccatc ccacctccag cactgaagc catctcagct 360
cataaaaaca actgcttgca aggcacaggt ttcttgagg aagagattac ccgggtcggg 420
gttctgtttg cttcaaaggc tgtgatgcaa cttctgggtc acccatcgt gggccctctc 480
accaacagga ttggatatca tatccccatg tttgctggct ttgttatcat gtttctctcc 540
acagttatgt ttgctttttc tgggacctat actctactct ttgtggcccg aacccttcaa 600
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gatgaccatg agagaggacg agccatggga actgctctgg ggggcctggc cttgggggtg 720
ctgggtgggag ctcccttttg aagtgtaatg tacgagtttg ttgggaagtc tgcacccttc 780
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tacatcctgg tggctgcagg gtccatctgc tttgccaaca tgggggtggc catcctggag 960
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ccccggcaa aggaagagaa gcttgctatt ctgagtcagg actgccccat ggagaccggg 1500
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<210> 7

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 7

Met	Arg	Thr	Leu	Asn	Thr	Ser	Ala	Met	Asp	Gly	Thr	Gly	Leu	Val	Val	1	5	10	15
Glu	Arg	Asp	Phe	Ser	Val	Arg	Ile	Leu	Thr	Ala	Cys	Phe	Leu	Ser	Leu	20	25	30	
Leu	Ile	Leu	Ser	Thr	Leu	Leu	Gly	Asn	Thr	Leu	Val	Cys	Ala	Ala	Val	35	40	45	
Ile	Arg	Phe	Arg	His	Leu	Arg	Ser	Lys	Val	Thr	Asn	Phe	Phe	Val	Ile	50	55	60	
Ser	Leu	Ala	Val	Ser	Asp	Leu	Leu	Val	Ala	Val	Leu	Val	Met	Pro	Trp	65	70	75	80
Lys	Ala	Val	Ala	Glu	Ile	Ala	Gly	Phe	Trp	Pro	Phe	Gly	Ser	Phe	Cys	85	90	95	
Asn	Ile	Trp	Val	Ala	Phe	Asp	Ile	Met	Cys	Ser	Thr	Ala	Ser	Ile	Leu	100	105	110	
Asn	Leu	Cys	Val	Ile	Ser	Val	Asp	Arg	Tyr	Trp	Ala	Ile	Ser	Ser	Pro	115	120	125	
Phe	Arg	Tyr	Glu	Arg	Lys	Met	Thr	Pro	Lys	Ala	Ala	Phe	Ile	Leu	Ile	130	135	140	
Ser	Val	Ala	Trp	Thr	Leu	Ser	Val	Leu	Ile	Ser	Phe	Ile	Pro	Val	Gln	145	150	155	160
Leu	Ser	Trp	His	Lys	Ala	Lys	Pro	Thr	Ser	Pro	Ser	Asp	Gly	Asn	Ala	165	170	175	
Thr	Ser	Leu	Ala	Glu	Thr	Ile	Asp	Asn	Cys	Asp	Ser	Ser	Leu	Ser	Arg	180	185	190	
Thr	Tyr	Ala	Ile	Ser	Ser	Ser	Val	Ile	Ser	Phe	Tyr	Ile	Pro	Val	Ala	195	200	205	
Ile	Met	Ile	Val	Thr	Tyr	Thr	Arg	Ile	Tyr	Arg	Ile	Ala	Gln	Lys	Gln	210	215	220	
Ile	Arg	Arg	Ile	Ala	Ala	Leu	Glu	Arg	Ala	Ala	Val	His	Ala	Lys	Asn	225	230	235	240
Cys	Gln	Thr	Thr	Thr	Gly	Asn	Gly	Lys	Pro	Val	Glu	Cys	Ser	Gln	Pro	245	250	255	
Glu	Ser	Ser	Phe	Lys	Met	Ser	Phe	Lys	Arg	Glu	Thr	Lys	Val	Leu	Lys	260	265	270	
Thr	Leu	Ser	Val	Ile	Met	Gly	Val	Phe	Val	Cys	Cys	Trp	Leu	Pro	Phe	275	280	285	
Phe	Ile	Leu	Asn	Cys	Ile	Leu	Pro	Phe	Cys	Gly	Ser	Gly	Glu	Thr	Gln	290	295	300	
Pro	Phe	Cys	Ile	Asp	Ser	Asn	Thr	Phe	Asp	Val	Phe	Val	Trp	Phe	Gly	305	310	315	320
Trp	Ala	Asn	Ser	Ser	Leu	Asn	Pro	Ile	Ile	Tyr	Ala	Phe	Asn	Ala	Asp	325	330	335	
Phe	Arg	Lys	Ala	Phe	Ser	Thr	Leu	Leu	Gly	Cys	Tyr	Arg	Leu	Cys	Pro	340	345	350	
Ala	Thr	Asn	Asn	Ala	Ile	Glu	Thr	Val	Ser	Ile	Asn	Asn	Asn	Gly	Ala	355	360	365	
Ala	Met	Phe	Ser	Ser	His	His	Glu	Pro	Arg	Gly	Ser	Ile	Ser	Lys	Glu	370	375	380	
Cys	Asn	Leu	Val	Tyr	Leu	Ile	Pro	His	Ala	Val	Gly	Ser	Ser	Glu	Asp	385	390	395	400
Leu	Lys	Lys	Glu	Glu	Ala	Ala	Gly	Ile	Ala	Arg	Pro	Leu	Glu	Lys	Leu	405	410	415	

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Ser Pro Ala Leu Ser Val Ile Leu Asp Tyr Asp Thr Asp Val Ser Leu
 420 425 430
 Glu Lys Ile Gln Pro Ile Thr Gln Asn Gly Gln His Pro Thr
 435 440 445

<210> 8
 <211> 1341
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 8
 atgaggactc tgaacacctc tgccatggac gggactgggc tgggtggtgga gagggacttc 60
 tctgttcgta tctcactgc ctgtttccta tcgctgctca tcctgtccac gtccttgggg 120
 aacacgctgg tctgtgctgc cgttatcagg ttccgacacc tgcggtccaa ggtgaccaac 180
 ttctttgtca tctccttggc tgtgtcagat ctcttgggtg cagtcttggg catgccctgg 240
 aaggcagtggt ctgagattgc tggcttcttg ccctttgggt ccttctgtaa catctgggtg 300
 gcctttgaca tcatgtgctc cactgcatcc atcctcaacc tctgtgtgat cagcgtggac 360
 aggtattggg ctatctccag ccctttccgg tatgagagaa agatgacccc caaggcagcc 420
 ttcatcctga tcagtgtggc atggaccttg tctgtactca tctccttcat ccagtgagc 480
 ctgagctggc acaaggcaaa acccacaagc ccctctgatg gaaatgccac ttccctggct 540
 gagaccatag acaactgtga ctccagcctc agcaggacat atgccatctc atcctctgta 600
 ataagctttt acatccctgt ggccatcatg attgtcacct acaccaggat ctacaggatt 660
 gtcagaaaac aaatacggcg cattgcgggc ttggagaggg cagcagtgcca cgccaagaat 720
 tgccagacca ccacaggtaa tggaaagcct gtcgaatgtt ctcaaccgga aagttctttt 780
 aagatgtcct tcaaaagaga aactaaagtc ctgaagactc tgtcggtgat catgggtgtg 840
 tttgtgtgct gttggctacc tttcttcac ttgaactgca ttttgccctt ctgtgggtct 900
 ggggagagcg agcccttctg cattgattcc aacacctttg acgtgtttgt gtgggttggg 960
 tgggctaatt catccttgaa ccccatcatt tatgccttta atgctgattt tcggaaggca 1020
 ttttcaacct tcttaggatg ctacagactt tgccctgcga cgaataatgc catagagacg 1080
 gtgagtatca ataacaatgg ggccgcgatg ttttccagcc atcatgagcc acgaggctcc 1140
 atctccaagg agtgcaatct ggtttacctg atcccacatg ctgtgggctc ctctgaggac 1200
 ctgaaaaagg aggaggcagc tggcatcgcc agacccttgg agaagctgtc cccagcccta 1260
 tcggtcatat tggactatga cactgacgtc tctctggaga agatccaacc catcacacaa 1320
 aacggtcagc acccaacctg a 1341

<210> 9
 <211> 443
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 9
 Met Asp Pro Leu Asn Leu Ser Trp Tyr Asp Asp Asp Leu Glu Arg Gln
 1 5 10 15
 Asn Trp Ser Arg Pro Phe Asn Gly Ser Asp Gly Lys Ala Asp Arg Pro
 20 25 30
 His Tyr Asn Tyr Tyr Ala Thr Leu Thr Leu Leu Ile Ala Val Ile
 35 40 45
 Val Phe Gly Asn Val Leu Val Cys Met Ala Val Ser Arg Glu Lys Ala
 50 55 60
 Leu Gln Thr Thr Thr Asn Tyr Leu Ile Val Ser Leu Ala Val Ala Asp
 65 70 75 80
 Leu Leu Val Ala Thr Leu Val Met Pro Trp Val Val Tyr Leu Glu Val
 85 90 95

Val	Gly	Glu	Trp	Lys	Phe	Ser	Arg	Ile	His	Cys	Asp	Ile	Phe	Val	Thr
			100					105					110		
Leu	Asp	Val	Met	Met	Cys	Thr	Ala	Ser	Ile	Leu	Asn	Leu	Cys	Ala	Ile
		115					120					125			
Ser	Ile	Asp	Arg	Tyr	Thr	Ala	Val	Ala	Met	Pro	Met	Leu	Tyr	Asn	Thr
	130					135				140					
Arg	Tyr	Ser	Ser	Lys	Arg	Arg	Val	Thr	Val	Met	Ile	Ser	Ile	Val	Trp
145				150						155					160
Val	Leu	Ser	Phe	Thr	Ile	Ser	Cys	Pro	Leu	Leu	Phe	Gly	Leu	Asn	Asn
				165				170						175	
Ala	Asp	Gln	Asn	Glu	Cys	Ile	Ile	Ala	Asn	Pro	Ala	Phe	Val	Val	Tyr
			180					185					190		
Ser	Ser	Ile	Val	Ser	Phe	Tyr	Val	Pro	Phe	Ile	Val	Thr	Leu	Leu	Val
		195					200					205			
Tyr	Ile	Lys	Ile	Tyr	Ile	Val	Leu	Arg	Arg	Arg	Arg	Lys	Arg	Val	Asn
	210					215					220				
Thr	Lys	Arg	Ser	Ser	Arg	Ala	Phe	Arg	Ala	His	Leu	Arg	Ala	Pro	Leu
225					230					235					240
Lys	Gly	Asn	Cys	Thr	His	Pro	Glu	Asp	Met	Lys	Leu	Cys	Thr	Val	Ile
				245				250						255	
Met	Lys	Ser	Asn	Gly	Ser	Phe	Pro	Val	Asn	Arg	Arg	Arg	Val	Glu	Ala
			260					265					270		
Ala	Arg	Arg	Ala	Gln	Glu	Leu	Glu	Met	Glu	Met	Leu	Ser	Ser	Thr	Ser
		275					280					285			
Pro	Pro	Glu	Arg	Thr	Arg	Tyr	Ser	Pro	Ile	Pro	Pro	Ser	His	His	Gln
		290				295					300				
Leu	Thr	Leu	Pro	Asp	Pro	Ser	His	His	Gly	Leu	His	Ser	Thr	Pro	Asp
305				310						315					320
Ser	Pro	Ala	Lys	Pro	Glu	Lys	Asn	Gly	His	Ala	Lys	Asp	His	Pro	Lys
			325						330					335	
Ile	Ala	Lys	Ile	Phe	Glu	Ile	Gln	Thr	Met	Pro	Asn	Gly	Lys	Thr	Arg
			340					345					350		
Thr	Ser	Leu	Lys	Thr	Met	Ser	Arg	Arg	Lys	Leu	Ser	Gln	Gln	Lys	Glu
		355					360					365			
Lys	Lys	Ala	Thr	Gln	Met	Leu	Ala	Ile	Val	Leu	Gly	Val	Phe	Ile	Ile
		370				375					380				
Cys	Trp	Leu	Pro	Phe	Phe	Ile	Thr	His	Ile	Leu	Asn	Ile	His	Cys	Asp
385				390						395					400
Cys	Asn	Ile	Pro	Pro	Val	Leu	Tyr	Ser	Ala	Phe	Thr	Trp	Leu	Gly	Tyr
			405						410					415	
Val	Asn	Ser	Ala	Val	Asn	Pro	Ile	Ile	Tyr	Thr	Thr	Phe	Asn	Ile	Glu
			420					425					430		
Phe	Arg	Lys	Ala	Phe	Leu	Lys	Ile	Leu	His	Cys					
		435					440								

<210> 10

<211> 1332

<212> DNA

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 10

atggatccac	tgaatctgtc	ctggtatgat	gatgatctgg	agaggcagaa	ctggagccgg	60
cccttcaacg	ggtcagacgg	gaaggcggac	agaccccact	acaactacta	tgccacactg	120
ctcaccctgc	tcatcgctgt	cattgtcttc	ggcaacgtgc	tggtgtgcat	ggctgtgtcc	180
cgcgagaagg	cgctgcagac	caccaccaac	tacctgatcg	tcagcctcgc	agtggccgac	240
ctctctcgtc	ccacatcggt	cattgccctgg	gttgtctacc	tggagggtgg	agtgagtggt	300
aaattcagca	ggattcactg	tgacatcttc	gtcactctgg	acgtctatgat	gtgcacggcg	360

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agcatcctga acttgtgtgc catcagcatc gacaggtaca cagctgtggc catgcccattg 420
ctgtacaata cgcgctacag ctccaagcgc cgggtcaccg tcatgatctc catcgtctgg 480
gtcctgtcct tcaccatctc ctgcccactc ctcttcggac tcaataacgc agaccagaac 540
gagtgcattca ttgccaaccc ggcttctgtg gtctactcct ccacgtctc cttctacgtg 600
cccttcattg tcaccctgct ggtctacatc aagatctaca ttgtcctccg cagacgccgc 660
aagcgagtca acaccaaacg cagcagccga gctttcaggg cccacctgag ggctccacta 720
aagggcaact gtactcacc caggagacatg aaactctgca ccgttatcat gaagtctaata 780
gggagtttcc cagtgaacag gcgagagtg gaggtgccc ggcgagccca ggagctggag 840
atggagatgc tctccagcac cagcccaccc gagaggacc ggtacagccc catcccaccc 900
agccaccacc agctgactct ccccgaccca tcccaccag gtctccacag cactcccgc 960
agccccgcca aaccagagaa gaatgggcat gccaaagacc accccaagat tgccaagatc 1020
tttgagatcc agaccatgcc caatggcaaa acccgacact ccctcaagac catgagccgt 1080
aggaagctct cccagcagaa ggagaagaaa gccactcaga tgctcgccat tgttctcggc 1140
gtgttcatca tctgctggct gcccttcttc atcacacaca tctgaacat acactgtgac 1200
tgcaacatcc cgcctgtcct gtacagcgcc ttcacgtggc tgggctatgt caacagcgcc 1260
gtgaacccca tcatctacac caccttcaac attgagttcc gcaaggcctt cctgaagatc 1320
ctccactgct ga 1332

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<210> 11

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 11

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Met Asp Pro Leu Asn Leu Ser Trp Tyr Asp Asp Asp Leu Glu Arg Gln
1           5           10           15
Asn Trp Ser Arg Pro Phe Asn Gly Ser Glu Gly Lys Ala Asp Arg Pro
20           25           30
His Tyr Asn Tyr Tyr Ala Met Leu Leu Thr Leu Leu Ile Phe Ile Ile
35           40           45
Val Phe Gly Asn Val Leu Val Cys Met Ala Val Ser Arg Glu Lys Ala
50           55           60
Leu Gln Thr Thr Thr Asn Tyr Leu Ile Val Ser Leu Ala Val Ala Asp
65           70           75           80
Leu Leu Val Ala Thr Leu Val Met Pro Trp Val Val Tyr Leu Glu Val
85           90           95
Val Gly Glu Trp Lys Phe Ser Arg Ile His Cys Asp Ile Phe Val Thr
100          105          110
Leu Asp Val Met Met Cys Thr Ala Ser Ile Leu Asn Leu Cys Ala Ile
115          120          125
Ser Ile Asp Arg Tyr Thr Ala Val Ala Met Pro Met Leu Tyr Asn Thr
130          135          140
Arg Tyr Ser Ser Lys Arg Arg Val Thr Val Met Ile Ala Ile Val Trp
145          150          155          160
Val Leu Ser Phe Thr Ile Ser Cys Pro Leu Leu Phe Gly Leu Asn Asn
165          170          175
Thr Asp Gln Asn Glu Cys Ile Ile Ala Asn Pro Ala Phe Val Val Tyr
180          185          190
Ser Ser Ile Val Ser Phe Tyr Val Pro Phe Ile Val Thr Leu Leu Val
195          200          205
Tyr Ile Lys Ile Tyr Ile Val Leu Arg Lys Arg Arg Lys Arg Val Asn
210          215          220
Thr Lys Arg Ser Ser Arg Ala Phe Arg Ala Asn Leu Lys Thr Pro Leu
225          230          235          240
Lys Gly Asn Cys Thr His Pro Glu Asp Met Lys Leu Cys Thr Val Ile
245          250          255

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Met Lys Ser Asn Gly Ser Phe Pro Val Asn Arg Arg Arg Met Asp Ala
      260                      265                      270
Ala Arg Arg Ala Gln Glu Leu Glu Met Glu Met Leu Ser Ser Thr Ser
      275                      280                      285
Pro Pro Glu Arg Thr Arg Tyr Ser Pro Ile Pro Pro Ser His His Gln
      290                      295                      300
Leu Thr Leu Pro Asp Pro Ser His His Gly Leu His Ser Asn Pro Asp
      305                      310                      315                      320
Ser Pro Ala Lys Pro Glu Lys Asn Gly His Ala Lys Ile Val Asn Pro
      325                      330                      335
Arg Ile Ala Lys Phe Phe Glu Ile Gln Thr Met Pro Asn Gly Lys Thr
      340                      345                      350
Arg Thr Ser Leu Lys Thr Met Ser Arg Arg Lys Leu Ser Gln Gln Lys
      355                      360                      365
Glu Lys Lys Ala Thr Gln Met Leu Ala Ile Val Leu Gly Val Phe Ile
      370                      375                      380
Ile Cys Trp Leu Pro Phe Phe Ile Thr His Ile Leu Asn Ile His Cys
      385                      390                      395                      400
Asp Cys Asn Ile Pro Pro Val Leu Tyr Ser Ala Phe Thr Trp Leu Gly
      405                      410                      415
Tyr Val Asn Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr Phe Asn Ile
      420                      425                      430
Glu Phe Arg Lys Ala Phe Met Lys Ile Leu His Cys
      435                      440

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<210> 12

<211> 1335

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 12

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atggatccac tgaacctgtc ctggtacgat gacgatctgg agaggcagaa ctggagccgg      60
cccttcaatg ggtcagaagg gaaggcagac agggcccact acaactacta tgccatgctg      120
ctcaccctcc tcactctttat catcgtcttt ggcaatgtgc tgggtgtgcat ggctgtatcc      180
cgagagaagg ctttgcagac caccaccaac tacttgatag tcagccttgc tgtggctgat      240
cttctgggtg ccacactggt aatgccgtgg gttgtctacc tggaggtggg ggggtgagtgg      300
aaattcagca ggattcactg tgacatcttt gtcactctgg atgtcatgat gtgcacagca      360
agcatcctga acctgtgtgc catcagcatt gacaggtaca cagctgtggc aatgcccatg      420
ctgtataaca cacgctacag ctccaagcgc cgagttactg tcatgattgc cattgtctgg      480
gtcctgtect tcaccatctc ctgcccactg ctcttcggac tcaacaatac agaccagaat      540
gagtgtatca ttgccaaacc tgccctttgtg gtctactcct ccattgtctc attctacgtg      600
cccttcacgc tcactctgct ggtctatatc aaaatctaca tcgtcctccg gaagcgccgg      660
aagcgggtca acaccaagcg cagcagtcga gctttcagag ccaacctgaa gacaccactc      720
aagggcaact gtaccacccc tgaggacatg aaactctgca ccgttatcat gaagtctaatt      780
gggagtttcc cagtgaacag ggggagaatg gatgctgcc gccgagctca ggagctggaa      840
atggagatgc tgtcaagcac cagtccccc gagaggaccc ggtatagccc catccctccc      900
agtcaccacc agctcactct cctgatcca tcccaccacg gcctacatag caaccctgac      960
agtccctgcc aaccagagaa gaatgggcac gccaaagatt tcaatcccag gattgccaaag      1020
ttctttgaga tccagaccat gcccaatggc aaaacccgga cctcccttaa gacgatgagc      1080
cgcagaaagc tctcccagca gaaggagaag aaagccactc agatgcttgc cattgttctc      1140
gggtgtgttc tcactgtctg gctgcccctt ttcatcacgc acatcctgaa tatacactgt      1200
gattgcaaca tcccaccagt cctctacagc gccttcacat ggctgggcta tgtcaacagt      1260
gccgtcaacc ccatcatcta caccaccttc aacatcgagt tccgcaaggc cttcatgaag      1320
atcttgcaat gctga

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<210> 13

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 13

Met	Asp	Pro	Leu	Asn	Leu	Ser	Trp	Tyr	Asp	Asp	Asp	Leu	Glu	Arg	Gln
1				5					10					15	
Asn	Trp	Ser	Arg	Pro	Phe	Asn	Gly	Ser	Glu	Gly	Lys	Ala	Asp	Arg	Pro
			20					25					30		
His	Tyr	Asn	Tyr	Tyr	Ala	Met	Leu	Leu	Thr	Leu	Leu	Ile	Phe	Ile	Ile
		35					40					45			
Val	Phe	Gly	Asn	Val	Leu	Val	Cys	Met	Ala	Val	Ser	Arg	Glu	Lys	Ala
	50					55					60				
Leu	Gln	Thr	Thr	Thr	Asn	Tyr	Leu	Ile	Val	Ser	Leu	Ala	Val	Ala	Asp
65					70					75					80
Leu	Leu	Val	Ala	Thr	Leu	Val	Met	Pro	Trp	Val	Val	Tyr	Leu	Glu	Val
				85					90					95	
Val	Gly	Glu	Trp	Lys	Phe	Ser	Arg	Ile	His	Cys	Asp	Ile	Phe	Val	Thr
			100					105					110		
Leu	Asp	Val	Met	Met	Cys	Thr	Ala	Ser	Ile	Leu	Asn	Leu	Cys	Ala	Ile
		115					120					125			
Ser	Ile	Asp	Arg	Tyr	Thr	Ala	Val	Ala	Met	Pro	Met	Leu	Tyr	Asn	Thr
	130					135					140				
Arg	Tyr	Ser	Ser	Lys	Arg	Arg	Val	Thr	Val	Met	Ile	Ala	Ile	Val	Trp
145				150						155					160
Val	Leu	Ser	Phe	Thr	Ile	Ser	Cys	Pro	Leu	Leu	Phe	Gly	Leu	Asn	Asn
				165					170					175	
Thr	Asp	Gln	Asn	Glu	Cys	Ile	Ile	Ala	Asn	Pro	Ala	Phe	Val	Val	Tyr
			180					185					190		
Ser	Ser	Ile	Val	Ser	Phe	Tyr	Val	Pro	Phe	Ile	Val	Thr	Leu	Leu	Val
		195					200					205			
Tyr	Ile	Lys	Ile	Tyr	Ile	Val	Leu	Arg	Lys	Arg	Arg	Lys	Arg	Val	Asn
	210					215					220				
Thr	Lys	Arg	Ser	Ser	Arg	Ala	Phe	Arg	Ala	Asn	Leu	Lys	Thr	Pro	Leu
225					230					235					240
Lys	Gly	Asn	Cys	Thr	His	Pro	Glu	Asp	Met	Lys	Leu	Cys	Thr	Val	Ile
				245					250					255	
Met	Lys	Ser	Asn	Gly	Ser	Phe	Pro	Val	Asn	Arg	Arg	Arg	Met	Asp	Ala
			260					265					270		
Ala	Arg	Arg	Ala	Gln	Glu	Leu	Glu	Met	Glu	Met	Leu	Ser	Ser	Thr	Ser
		275					280					285			
Pro	Pro	Glu	Arg	Thr	Arg	Tyr	Ser	Pro	Ile	Pro	Pro	Ser	His	His	Gln
	290					295					300				
Leu	Thr	Leu	Pro	Asp	Pro	Ser	His	His	Gly	Leu	His	Ser	Asn	Pro	Asp
305					310					315					320
Ser	Pro	Ala	Lys	Pro	Glu	Lys	Asn	Gly	His	Ala	Lys	Ile	Val	Asn	Pro
				325					330					335	
Arg	Ile	Ala	Lys	Phe	Phe	Glu	Ile	Gln	Thr	Met	Pro	Asn	Gly	Lys	Thr
			340					345					350		
Arg	Thr	Ser	Leu	Lys	Thr	Met	Ser	Arg	Arg	Lys	Leu	Ser	Gln	Gln	Lys
		355					360					365			
Glu	Lys	Lys	Ala	Thr	Gln	Met	Leu	Ala	Ile	Val	Leu	Gly	Val	Phe	Ile
	370					375					380				
Ile	Cys	Trp	Leu	Pro	Phe	Phe	Ile	Thr	His	Ile	Leu	Asn	Ile	His	Cys
385					390					395					400
Asp	Cys	Asn	Ile	Pro	Pro	Val	Leu	Tyr	Ser	Ala	Phe	Thr	Trp	Leu	Gly
				405					410					415	

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Tyr Val Asn Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr Phe Asn Ile
 420 425 430
 Glu Phe Arg Lys Ala Phe Met Lys Ile Leu His Cys
 435 440

<210> 14
 <211> 619
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 14
 Met Ser Lys Ser Lys Cys Ser Val Gly Pro Met Ser Ser Val Val Ala
 1 5 10 15
 Pro Ala Lys Glu Pro Asn Ala Val Gly Pro Arg Glu Val Glu Leu Ile
 20 25 30
 Leu Val Lys Glu Gln Asn Gly Val Gln Leu Thr Asn Ser Thr Leu Ile
 35 40 45
 Asn Pro Pro Gln Thr Pro Val Glu Val Gln Glu Arg Glu Thr Trp Ser
 50 55 60
 Lys Lys Ile Asp Phe Leu Leu Ser Val Ile Gly Phe Ala Val Asp Leu
 65 70 75 80
 Ala Asn Val Trp Arg Phe Pro Tyr Leu Cys Tyr Lys Asn Gly Gly Gly
 85 90 95
 Ala Phe Leu Val Pro Tyr Leu Leu Phe Met Val Ile Ala Gly Met Pro
 100 105 110
 Leu Phe Tyr Met Glu Leu Ala Leu Gly Gln Phe Asn Arg Glu Gly Ala
 115 120 125
 Ala Gly Val Trp Lys Ile Cys Pro Val Leu Lys Gly Val Gly Phe Thr
 130 135 140
 Val Ile Leu Ile Ser Phe Tyr Val Gly Phe Phe Tyr Asn Val Ile Ile
 145 150 155 160
 Ala Trp Ala Leu His Tyr Phe Phe Ser Ser Phe Thr Met Asp Leu Pro
 165 170 175
 Trp Ile His Cys Asn Asn Thr Trp Asn Ser Pro Asn Cys Ser Asp Ala
 180 185 190
 His Ser Ser Asn Ser Ser Asp Gly Leu Gly Leu Asn Asp Thr Phe Gly
 195 200 205
 Thr Thr Pro Ala Ala Glu Tyr Phe Glu Arg Gly Val Leu His Leu His
 210 215 220
 Gln Ser Arg Gly Ile Asp Asp Leu Gly Pro Pro Arg Trp Gln Leu Thr
 225 230 235 240
 Ala Cys Leu Val Leu Val Ile Val Leu Leu Tyr Phe Ser Leu Trp Lys
 245 250 255
 Gly Val Lys Thr Ser Gly Lys Val Val Trp Ile Thr Ala Thr Met Pro
 260 265 270
 Tyr Val Val Leu Thr Ala Leu Leu Leu Arg Gly Val Thr Leu Pro Gly
 275 280 285
 Ala Met Asp Gly Ile Arg Ala Tyr Leu Ser Val Asp Phe Tyr Arg Leu
 290 295 300
 Cys Glu Ala Ser Val Trp Ile Asp Ala Ala Thr Gln Val Cys Phe Ser
 305 310 315 320
 Leu Gly Val Gly Phe Gly Val Leu Ile Ala Phe Ser Ser Tyr Asn Lys
 325 330 335
 Phe Thr Asn Asn Cys Tyr Arg Asp Ala Ile Ile Thr Thr Ser Ile Asn
 340 345 350
 Ser Leu Thr Ser Phe Ser Ser Gly Phe Val Val Phe Ser Phe Leu Gly
 355 360 365

Tyr Met Ala Gln Lys His Asn Val Pro Ile Arg Asp Val Ala Thr Asp
 370 375 380
 Gly Pro Gly Leu Ile Phe Ile Ile Tyr Pro Glu Ala Ile Ala Thr Leu
 385 390 395 400
 Pro Leu Ser Ser Ala Trp Ala Ala Val Phe Phe Leu Met Leu Leu Thr
 405 410 415
 Leu Gly Ile Asp Ser Ala Met Gly Gly Met Glu Ser Val Ile Thr Gly
 420 425 430
 Leu Val Asp Glu Phe Gln Leu Leu His Arg His Arg Glu Leu Phe Thr
 435 440 445
 Leu Gly Ile Val Leu Ala Thr Phe Leu Leu Ser Leu Phe Cys Val Thr
 450 455 460
 Asn Gly Gly Ile Tyr Val Phe Thr Leu Leu Asp His Phe Ala Ala Gly
 465 470 475 480
 Thr Ser Ile Leu Phe Gly Val Leu Ile Glu Ala Ile Gly Val Ala Trp
 485 490 495
 Phe Tyr Gly Val Gln Gln Phe Ser Asp Asp Ile Lys Gln Met Thr Gly
 500 505 510
 Gln Arg Pro Asn Leu Tyr Trp Arg Leu Cys Trp Lys Leu Val Ser Pro
 515 520 525
 Cys Phe Leu Leu Tyr Val Val Val Ser Ile Val Thr Phe Arg Pro
 530 535 540
 Pro His Tyr Gly Ala Tyr Ile Phe Pro Asp Trp Ala Asn Ala Leu Gly
 545 550 555 560
 Trp Ile Ile Ala Thr Ser Ser Met Ala Met Val Pro Ile Tyr Ala Thr
 565 570 575
 Tyr Lys Phe Cys Ser Leu Pro Gly Ser Phe Arg Glu Lys Leu Ala Tyr
 580 585 590
 Ala Ile Thr Pro Glu Lys Asp Arg Gln Leu Val Asp Arg Gly Glu Val
 595 600 605
 Arg Gln Phe Thr Leu Arg His Trp Leu Leu Val
 610 615

<210> 15

<211> 619

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 15

Met Ser Lys Ser Lys Cys Ser Val Gly Pro Met Ser Ser Val Val Ala
 1 5 10 15
 Pro Ala Lys Glu Ser Asn Ala Val Gly Pro Arg Glu Val Glu Leu Ile
 20 25 30
 Leu Val Lys Glu Gln Asn Gly Val Gln Leu Thr Asn Ser Thr Leu Ile
 35 40 45
 Asn Pro Pro Gln Thr Pro Val Glu Ala Gln Glu Arg Glu Thr Trp Ser
 50 55 60
 Lys Lys Ile Asp Phe Leu Leu Ser Val Ile Gly Phe Ala Val Asp Leu
 65 70 75 80
 Ala Asn Val Trp Arg Phe Pro Tyr Leu Cys Tyr Lys Asn Gly Gly Gly
 85 90 95
 Ala Phe Leu Val Pro Tyr Leu Leu Phe Met Val Ile Ala Gly Met Pro
 100 105 110
 Leu Phe Tyr Met Glu Leu Ala Leu Gly Gln Phe Asn Arg Glu Gly Ala
 115 120 125
 Ala Gly Val Trp Lys Ile Cys Pro Val Leu Lys Gly Val Gly Phe Thr
 130 135 140

Val	Ile	Leu	Ile	Ser	Phe	Tyr	Val	Gly	Phe	Phe	Tyr	Asn	Val	Ile	Ile	145	150	155	160
Ala	Trp	Ala	Leu	His	Tyr	Phe	Phe	Ser	Ser	Phe	Thr	Met	Asp	Leu	Pro	165	170		175
Trp	Ile	His	Cys	Asn	Asn	Thr	Trp	Asn	Ser	Pro	Asn	Cys	Ser	Asp	Ala	180	185		190
His	Ala	Ser	Asn	Ser	Ser	Asp	Gly	Leu	Gly	Leu	Asn	Asp	Thr	Phe	Gly	195	200	205	
Thr	Thr	Pro	Ala	Ala	Glu	Tyr	Phe	Glu	Arg	Gly	Val	Leu	His	Leu	His	210	215	220	
Gln	Ser	Arg	Gly	Ile	Asp	Asp	Leu	Gly	Pro	Pro	Arg	Trp	Gln	Leu	Thr	225	230	235	240
Ala	Cys	Leu	Val	Leu	Val	Ile	Val	Leu	Leu	Tyr	Phe	Ser	Leu	Trp	Lys	245	250		255
Gly	Val	Lys	Thr	Ser	Gly	Lys	Val	Val	Trp	Ile	Thr	Ala	Thr	Met	Pro	260	265		270
Tyr	Val	Val	Leu	Thr	Ala	Leu	Leu	Leu	Arg	Gly	Val	Thr	Leu	Pro	Gly	275	280	285	
Ala	Met	Asp	Gly	Ile	Arg	Ala	Tyr	Leu	Ser	Val	Asp	Phe	Tyr	Arg	Leu	290	295	300	
Cys	Glu	Ala	Ser	Val	Trp	Ile	Asp	Ala	Ala	Thr	Gln	Val	Cys	Phe	Ser	305	310	315	320
Leu	Gly	Val	Gly	Phe	Gly	Val	Leu	Ile	Ala	Phe	Ser	Ser	Tyr	Asn	Lys	325	330		335
Phe	Thr	Asn	Asn	Cys	Tyr	Arg	Asp	Ala	Ile	Ile	Thr	Thr	Ser	Ile	Asn	340	345		350
Ser	Leu	Thr	Ser	Phe	Ser	Ser	Gly	Phe	Val	Val	Phe	Ser	Phe	Leu	Gly	355	360	365	
Tyr	Met	Ala	Gln	Lys	His	Asn	Val	Pro	Ile	Arg	Asp	Val	Ala	Thr	Asp	370	375	380	
Gly	Pro	Gly	Leu	Ile	Phe	Ile	Ile	Tyr	Pro	Glu	Ala	Ile	Ala	Thr	Leu	385	390	395	400
Pro	Leu	Ser	Ser	Ala	Trp	Ala	Ala	Val	Phe	Phe	Leu	Met	Leu	Leu	Thr	405	410		415
Leu	Gly	Ile	Asp	Ser	Ala	Met	Gly	Gly	Met	Glu	Ser	Val	Ile	Thr	Gly	420	425	430	
Leu	Val	Asp	Glu	Phe	Gln	Leu	Leu	His	Arg	His	Arg	Glu	Leu	Phe	Thr	435	440	445	
Leu	Gly	Ile	Val	Leu	Ala	Thr	Phe	Leu	Leu	Ser	Leu	Phe	Cys	Val	Thr	450	455	460	
Asn	Gly	Gly	Ile	Tyr	Val	Phe	Thr	Leu	Leu	Asp	His	Phe	Ala	Ala	Gly	465	470	475	480
Thr	Ser	Ile	Leu	Phe	Gly	Val	Leu	Ile	Glu	Ala	Ile	Gly	Val	Ala	Trp	485	490		495
Phe	Tyr	Gly	Val	Gln	Gln	Phe	Ser	Asp	Asp	Ile	Lys	Gln	Met	Thr	Gly	500	505	510	
Gln	Arg	Pro	Asn	Leu	Tyr	Trp	Arg	Leu	Cys	Trp	Lys	Leu	Val	Ser	Pro	515	520	525	
Cys	Phe	Leu	Leu	Tyr	Val	Val	Val	Val	Ser	Ile	Val	Thr	Phe	Arg	Pro	530	535	540	
Pro	His	Tyr	Gly	Ala	Tyr	Ile	Phe	Pro	Asp	Trp	Ala	Asn	Ala	Leu	Gly	545	550	555	560
Trp	Ile	Ile	Ala	Thr	Ser	Ser	Met	Ala	Met	Val	Pro	Ile	Tyr	Ala	Thr	565	570		575
Tyr	Lys	Phe	Cys	Ser	Leu	Pro	Gly	Ser	Phe	Arg	Glu	Lys	Leu	Ala	Tyr	580	585	590	
Ala	Ile	Thr	Pro	Glu	Lys	Asp	His	Gln	Leu	Val	Asp	Arg	Gly	Glu	Val	595	600	605	
Arg	Gln	Phe	Thr	Leu	Arg	His	Trp	Leu	Leu	Leu						610	615		

<210> 16
 <211> 620
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 16
 Met Ser Lys Ser Lys Cys Ser Val Gly Leu Met Ser Ser Val Val Ala
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 Pro Ala Lys Glu Pro Asn Ala Val Gly Pro Lys Glu Val Glu Leu Ile
 20 25 30
 Leu Val Lys Glu Gln Asn Gly Val Gln Leu Thr Ser Ser Thr Leu Thr
 35 40 45
 Asn Pro Arg Gln Ser Pro Val Glu Ala Gln Asp Arg Glu Thr Trp Gly
 50 55 60
 Lys Lys Ile Asp Phe Leu Leu Ser Val Ile Gly Phe Ala Val Asp Leu
 65 70 75 80
 Ala Asn Val Trp Arg Phe Pro Tyr Leu Cys Tyr Lys Asn Gly Gly Gly
 85 90 95
 Ala Phe Leu Val Pro Tyr Leu Leu Phe Met Val Ile Ala Gly Met Pro
 100 105 110
 Leu Phe Tyr Met Glu Leu Ala Leu Gly Gln Phe Asn Arg Glu Gly Ala
 115 120 125
 Ala Gly Val Trp Lys Ile Cys Pro Ile Leu Lys Gly Val Gly Phe Thr
 130 135 140
 Val Ile Leu Ile Ser Leu Tyr Val Gly Phe Phe Tyr Asn Val Ile Ile
 145 150 155 160
 Ala Trp Ala Leu His Tyr Leu Phe Ser Ser Phe Thr Thr Glu Leu Pro
 165 170 175
 Trp Ile His Cys Asn Asn Ser Trp Asn Ser Pro Asn Cys Ser Asp Ala
 180 185 190
 His Pro Gly Asp Ser Ser Gly Asp Ser Ser Gly Leu Asn Asp Thr Phe
 195 200 205
 Gly Thr Thr Pro Ala Ala Glu Tyr Phe Glu Arg Gly Val Leu His Leu
 210 215 220
 His Gln Ser His Gly Ile Asp Asp Leu Gly Pro Pro Arg Trp Gln Leu
 225 230 235 240
 Thr Ala Cys Leu Val Leu Val Ile Val Leu Leu Tyr Phe Ser Leu Trp
 245 250 255
 Lys Gly Val Lys Thr Ser Gly Lys Val Val Trp Ile Thr Ala Thr Met
 260 265 270
 Pro Tyr Val Val Leu Thr Ala Leu Leu Leu Arg Gly Val Thr Leu Pro
 275 280 285
 Gly Ala Ile Asp Gly Ile Arg Ala Tyr Leu Ser Val Asp Phe Tyr Arg
 290 295 300
 Leu Cys Glu Ala Ser Val Trp Ile Asp Ala Ala Thr Gln Val Cys Phe
 305 310 315 320
 Ser Leu Gly Val Gly Phe Gly Val Leu Ile Ala Phe Ser Ser Tyr Asn
 325 330 335
 Lys Phe Thr Asn Asn Cys Tyr Arg Asp Ala Ile Val Thr Thr Ser Ile
 340 345 350
 Asn Ser Leu Thr Ser Phe Ser Ser Gly Phe Val Val Phe Ser Phe Leu
 355 360 365
 Gly Tyr Met Ala Gln Lys His Ser Val Pro Ile Gly Asp Val Ala Lys
 370 375 380
 Asp Gly Pro Gly Leu Ile Phe Ile Ile Tyr Pro Glu Ala Ile Ala Thr
 385 390 395 400


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Leu Pro Leu Ser Ser Ala Trp Ala Val Val Phe Phe Ile Met Leu Leu
              405                      410                      415
Thr Leu Gly Ile Asp Ser Ala Met Gly Gly Met Glu Ser Val Ile Thr
              420                      425                      430
Gly Leu Ile Asp Glu Phe Gln Leu Leu His Arg His Arg Glu Leu Phe
              435                      440                      445
Thr Leu Phe Ile Val Leu Ala Thr Phe Leu Leu Ser Leu Phe Cys Val
              450                      455                      460
Thr Asn Gly Gly Ile Tyr Val Phe Thr Leu Leu Asp His Phe Ala Ala
465              470                      475                      480
Gly Thr Ser Ile Leu Phe Gly Val Leu Ile Glu Ala Ile Gly Val Ala
              485                      490                      495
Trp Phe Tyr Gly Val Gly Gln Phe Ser Asp Asp Ile Gln Gln Met Thr
              500                      505                      510
Gly Gln Arg Pro Ser Leu Tyr Trp Arg Leu Cys Trp Lys Leu Val Ser
              515                      520                      525
Pro Cys Phe Leu Leu Phe Val Val Val Val Ser Ile Val Thr Phe Arg
530              535                      540
Pro Pro His Tyr Gly Ala Tyr Ile Phe Pro Asp Trp Ala Asn Ala Leu
545              550                      555                      560
Gly Trp Val Ile Ala Thr Ser Ser Met Ala Met Val Pro Ile Tyr Ala
              565                      570                      575
Ala Tyr Lys Phe Cys Ser Leu Pro Gly Ser Phe Arg Glu Lys Leu Ala
              580                      585                      590
Tyr Ala Ile Ala Pro Glu Lys Asp Arg Glu Leu Val Asp Arg Gly Glu
595              600                      605
Val Arg Gln Phe Thr Leu Arg His Trp Leu Lys Val
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<210> 17

<211> 1873

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 17

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gagtgcagct gaccaattcc accctcatca acccaccgca gacaccagtg gaggttcaag      180
agcgggagac ctggagcaag aaaatcgatt tcctgtcttc agtcatcggc ttcgctgtgg      240
acctggccaa tgtttgagg tttccctacc tgtgctacaa aaatgggtgga ggtgccttcc      300
tggtgcccta cctgctcttc atggttattg ccgggatgcc cctctttctac atggagctgg      360
ctctcgggca gttcaacaga gaaggagctg ctggtgtctg gaagatctgc cctgtcctga      420
aagggtgtgg cttcactgtc atcctcatct cttctacgt gggcttcttc tacaatgtca      480
tcattgcatg ggcactgcac tacttcttct cctccttcac catggacctc ccatggatcc      540
actgcaacaa cacctggaac agccccaact gttctgatgc acatagcagc aactctagcg      600
atggcctggg cctcaacgac acctttggga ccacaccgc tgctgagtat tttgagcgtg      660
gtgtgctgca cctccatcag agtcgtggca ttgatgacct gggccctcca cgggtggcagc      720
tcacagcctg cctggtgctg gtcattgttc tgctctactt cagcctgtgg aaggaggtaa      780
agacttcagg gaagggtggg tggatcacag ctaccatgcc ctatgtagtc ctcacagccc      840
tgctcctgcg tggagtcacc ctccctgggg ccatggatgg catcagagca tacctcagtg      900
tggaattcta cgtctctgt gaggcactct tgggatcga tgccgccacc cagggtgtgct      960
tctcccttgg cgttgggttt ggggtgctga ttgccttctc cagttacaat aagttcacca      1020
ataactgcta tagagatgca atcatcacca cctccattaa ctccctgacg agcttctcct      1080
ctggcttcgt tgtcttctcc ttccctgggg acatggcaca gaagcacaat gtgcccataca      1140
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cactcccgtg gtcttcagcc tgggcccgtg tcttcttctc catgctgtct actctgggta      1260
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tgctacatcg	gcategagag	ctcttcactc	ttggcattgt	cctggctact	ttcctgctgt	1380
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ctggcacatc	tatcctcttt	ggagtgcaca	ttgaagccat	tgggggtggc	tgggtctacg	1500
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tctgcagcct	gccaggggtcc	ttccgagaga	aactggccta	tgccatcaca	cctgagaaa	1800
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<210> 18

<211> 2020

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 18

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ccttgtcatg	gagcagaacg	gagtgcagct	caccagctcc	accctcacca	acccgcggca	180
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cgtcattggc	tttgcgtgtg	acctggccaa	cgtctggagg	ttcccctacc	tgtgctacaa	300
aaatgggtggc	ggtgccttcc	tgggtccccta	cctgctcttc	atgggtcattg	ctgggatgcc	360
acttttctac	atggagctgg	ccctcggcca	gttcaacagg	gaagggggccg	ctgggtgtctg	420
gaagatctgc	cccatactga	aagggtgtggg	cttcacggtc	atcctcatct	cactgtatgt	480
cggcttcttc	tacaacgtca	tcatcgctg	ggcgtgcac	tatctcttct	cctccttcac	540
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catcggagtg	gcctggttct	atggtgttgg	gcagttcagc	gacgacatcc	agcagatgac	1560
cgggcagcgg	cccagcctgt	actggcggct	gtgctggaag	ctggtcagcc	cctgcttctt	1620
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